SEQUENCE LISTING

<110> Fritz, Christian
      Youngman, Philip

<120> USE OF YNES, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES

<130> 06286-090001

<140> US 09/163,445
<141> 1998-09-30

<150> US 60/070,116
<151> 1997-12-31

<160> 12

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 213
<212> PRT
<213> Streptococcus pneumoniae

<400> 1
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1   5   10   15
Pro Ser Gly Leu Trp Ile Gly Gln Val Phe Phe Gln Ile Asn Leu Arg
            20   25   30
Glu His Gly Ser Gly Asn Thr Gly Thr Thr Asn Thr Phe Arg Ile Leu
            35   40   45
Gly Lys Lys Ala Gly Met Ala Thr Phe Val Ile Asp Phe Phe Lys Gly
        50   55   60
Thr Leu Ala Thr Leu Leu Pro Ile Ile Phe His Leu Gln Gly Val Ser
65   70   75   80
Pro Leu Ile Phe Gly Leu Leu Ala Val Ile Gly His Thr Phe Pro Ile
                85   90   95
Phe Ala Gly Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Ala Gly Val
                100   105   110
Ile Phe Gly Phe Ala Pro Ile Phe Cys Leu Tyr Leu Ala Ile Ile Phe
                115   120   125
Phe Gly Ala Leu Tyr Leu Gly Ser Met Ile Ser Leu Ser Ser Val Thr
        130   135   140
Ala Ser Ile Ala Ala Val Ile Gly Val Leu Leu Phe Pro Leu Phe Gly
145   150   155   160
Phe Ile Leu Ser Asn Tyr Asp Ser Leu Phe Ile Ala Ile Ile Leu Ala
                165   170   175
Leu Ala Ser Leu Ile Ile Ile Arg His Lys Asp Asn Ile Ala Arg Ile
                180   185   190
Lys Asn Lys Thr Glu Asn Leu Val Pro Trp Gly Leu Asn Leu Thr His
        195   200   205
Gln Asp Pro Lys Lys
        210

<210> 2
<211> 642

<212> DNA
<213> Streptococcus pneumoniae

<220>
<221> CDS
<222> (1)...(639)

<400> 2

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Met Ile Thr Ile Val Leu Leu Ile Leu Ala Tyr Leu Leu Gly Ser Ile
1               5                   10                  15

cca tct ggt ctc tgg att gga caa gta ttc ttt caa atc aat cta cgc        96
Pro Ser Gly Leu Trp Ile Gly Gln Val Phe Phe Gln Ile Asn Leu Arg
            20                  25                  30

gag cat ggt tct ggt aac act gga acg acc aac acc ttc cgc att tta       144
Glu His Gly Ser Gly Asn Thr Gly Thr Thr Asn Thr Phe Arg Ile Leu
            35                  40                  45

ggt aag aaa gct ggt atg gca acc ttt gtg att gac ttt ttc aaa gga       192
Gly Lys Lys Ala Gly Met Ala Thr Phe Val Ile Asp Phe Phe Lys Gly
        50                  55                  60

acc cta gca acg ctg ctt ccg att att ttt cat cta caa ggc gtt tct       240
Thr Leu Ala Thr Leu Leu Pro Ile Ile Phe His Leu Gln Gly Val Ser
65                  70                  75                  80

cct ctc atc ttt gga ctt ttg gct gtt atc ggc cat acc ttc cct atc       288
Pro Leu Ile Phe Gly Leu Leu Ala Val Ile Gly His Thr Phe Pro Ile
                85                  90                  95

ttt gca gga ttt aaa ggt ggt aag gct gtc gca acc agt gct gga gtg       336
Phe Ala Gly Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Ala Gly Val
                100                 105                 110

att ttc gga ttt gcg cct atc ttc tgt ctc tac ctt gcg att atc ttc       384
Ile Phe Gly Phe Ala Pro Ile Phe Cys Leu Tyr Leu Ala Ile Ile Phe
                115                 120                 125

ttt gga gct ctc tat ctt ggc agt atg att tca ctg tct agt gtc aca       432
Phe Gly Ala Leu Tyr Leu Gly Ser Met Ile Ser Leu Ser Ser Val Thr
        130                 135                 140

gca tcg att gcg gct gtt atc ggg gtt ctg ctc ttt cca ctt ttt ggt       480
Ala Ser Ile Ala Ala Val Ile Gly Val Leu Leu Phe Pro Leu Phe Gly
145                 150                 155                 160

ttt atc ctg agt aac tat gac tct ctc ttc atc gct att atc tta gca       528
Phe Ile Leu Ser Asn Tyr Asp Ser Leu Phe Ile Ala Ile Ile Leu Ala
                165                 170                 175

ctt gct agt ttg att atc att cgt cat aag gac aat ata gct cgt atc       576
Leu Ala Ser Leu Ile Ile Ile Arg His Lys Asp Asn Ile Ala Arg Ile
                180                 185                 190

aaa aat aaa act gaa aat ttg gtc cct tgg gga ttg aac cta acc cat       624
```

```
Lys Asn Lys Thr Glu Asn Leu Val Pro Trp Gly Leu Asn Leu Thr His
        195             200             205

caa gat cct aaa aaa taa                                          642
Gln Asp Pro Lys Lys
        210
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<210> 3
<211> 193
<212> PRT
<213> Bacillus subtilis

<400> 3
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Met Leu Ile Ala Leu Leu Ile Ile Leu Ala Tyr Leu Ile Gly Ser Ile
 1               5              10              15
Pro Ser Gly Leu Ile Val Gly Lys Leu Ala Lys Gly Ile Asp Ile Arg
            20              25              30
Glu His Gly Ser Gly Asn Leu Gly Ala Thr Asn Ala Phe Arg Thr Leu
        35              40              45
Gly Val Lys Ala Gly Ser Val Val Ile Ala Gly Asp Ile Leu Lys Gly
    50              55              60
Thr Leu Ala Thr Ala Leu Pro Phe Leu Met His Val Asp Ile His Pro
 65              70              75              80
Leu Leu Ala Gly Val Phe Ala Val Leu Gly His Val Phe Pro Ile Phe
                85              90              95
Ala Lys Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Gly Gly Val Leu
            100             105             110
Leu Phe Tyr Ala Pro Leu Leu Phe Ile Thr Met Val Ala Val Phe Phe
        115             120             125
Ile Phe Leu Tyr Leu Thr Lys Phe Val Ser Leu Ser Ser Met Leu Thr
        130             135             140
Gly Ile Tyr Thr Val Ile Tyr Ser Phe Phe Val His Asp Thr Tyr Leu
145             150             155             160
Leu Ile Val Val Thr Leu Leu Thr Ile Phe Val Ile Tyr Arg His Arg
                165             170             175
Ala Asn Ile Lys Arg Ile Ile Asn Lys Thr Glu Pro Lys Val Lys Trp
            180             185             190
Leu
```

<210> 4
<211> 582
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)...(579)

<400> 4
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atg tta att gct tta ttg att att ttg gcc tac ttg ata ggc agc att    48
Met Leu Ile Ala Leu Leu Ile Ile Leu Ala Tyr Leu Ile Gly Ser Ile
 1               5              10              15

cca tct ggc tta att gtg ggc aag ctt gcc aaa gga att gat att cgg    96
Pro Ser Gly Leu Ile Val Gly Lys Leu Ala Lys Gly Ile Asp Ile Arg
            20              25              30
```

```
gag cac gga agc ggc aac tta ggc gct acc aat gca ttc cgt aca ttg      144
Glu His Gly Ser Gly Asn Leu Gly Ala Thr Asn Ala Phe Arg Thr Leu
         35                  40                  45

ggt gta aaa gct ggt tcg gtc gtc ata gcc gga gat att ttg aaa ggg      192
Gly Val Lys Ala Gly Ser Val Val Ile Ala Gly Asp Ile Leu Lys Gly
     50                  55                  60

aca ctg gca act gca ttg cct ttt ctc atg cat gtt gat att cac ccg      240
Thr Leu Ala Thr Ala Leu Pro Phe Leu Met His Val Asp Ile His Pro
 65                  70                  75                  80

ctt ctt gca gga gtc ttt gcg gtt tta ggc cac gtg ttt ccc atc ttc      288
Leu Leu Ala Gly Val Phe Ala Val Leu Gly His Val Phe Pro Ile Phe
                 85                  90                  95

gcc aaa ttt aaa ggc ggt aaa gcc gtg gcg aca tca gga ggc gtt ttg      336
Ala Lys Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Gly Gly Val Leu
             100                 105                 110

cta ttt tac gca ccc ctg tta ttt atc acg atg gtt gcg gta ttc ttc      384
Leu Phe Tyr Ala Pro Leu Leu Phe Ile Thr Met Val Ala Val Phe Phe
         115                 120                 125

atc ttt tta tac ttg act aaa ttt gtt tct ctc tca tcg atg tta aca      432
Ile Phe Leu Tyr Leu Thr Lys Phe Val Ser Leu Ser Ser Met Leu Thr
         130                 135                 140

ggg atc tat act gtt ata tat agt ttc ttt gtc cat gat acg tat tta      480
Gly Ile Tyr Thr Val Ile Tyr Ser Phe Phe Val His Asp Thr Tyr Leu
145                 150                 155                 160

ttg att gtc gtt acc ctg ctc act att ttt gtg ata tac aga cac cga      528
Leu Ile Val Val Thr Leu Leu Thr Ile Phe Val Ile Tyr Arg His Arg
                 165                 170                 175

gcg aac att aaa cga att atc aat aaa aca gaa cct aaa gta aaa tgg      576
Ala Asn Ile Lys Arg Ile Ile Asn Lys Thr Glu Pro Lys Val Lys Trp
             180                 185                 190

tta taa                                                              582
Leu
```

```
<210> 5
<211> 21
<212> DNA
<213> Bacillus subtilis

<400> 5
 gtgttcgtgc tgacttgcac c                                             21

<210> 6
<211> 21
<212> DNA
<213> Bacillus subtilis

<400> 6
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```
gaattatttc ctcccgttaa a                                                    21
```

```
<210> 7
<211> 21
<212> DNA
<213> Steptococcus pneumoniae
```

```
<400> 7
 acccactccg tgaagtccac c                                                    21
```

```
<210> 8
<211> 21
<212> DNA
<213> Streptococcus pneumoniae
```

```
<400> 8
 gaacccagca gataggctag g                                                    21
```

```
<210> 9
<211> 21
<212> DNA
<213> Steptococcus pneumoniae
```

```
<400> 9
 gaacctaacc catcaagatc c                                                    21
```

```
<210> 10
<211> 24
<212> DNA
<213> Streptococcus pneumoniae
```

```
<400> 10
 cagttttaga tggctttaac agcg                                                 24
```

```
<210> 11
<211> 642
<212> DNA
<213> Streptococcus pneumoniae
```

```
<400> 11
ttattttta ggatcttgat gggttaggtt caatccccaa gggaccaaat tttcagtttt       60
atttttgata cgagctatat tgtccttatg acgaatgata atcaaactag caagtgctaa      120
gataatagcg atgaagagag agtcatagtt actcaggata aaaccaaaaa gtggaaagag      180
cagaaccccg ataacagccg caatcgatgc tgtgacacta gacagtgaaa tcatactgcc      240
aagatagaga gctccaaaga agataatcgc aaggtagaga cagaagatag gcgcaaatcc      300
gaaaatcact ccagcactgg ttgcgacagc cttaccacct ttaaatcctg caaagatagg      360
gaaggtatgg ccgataacag ccaaaagtcc aaagatgaga ggagaaacgc cttgtagatg      420
aaaaataatc ggaagcagcg ttgctagggt tcctttgaaa aagtcaatca caaaggttgc      480
cataccagct ttcttaccta aaatgcggaa ggtgttggtc gttccagtgt taccagaacc      540
atgctcgcgt agattgattt gaaagaatac ttgtccaatc cagagaccag atggaatcga      600
acccagcaga taggctagga ttaataaaac tattgtaatc at                         642
```

```
<210> 12
<211> 582
<212> DNA
<213> Bacillus subtilis
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<400> 12

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aaagaaacta tatataacag tatagatccc tgttaacatc gatgagagag aaacaaattt         180
agtcaagtat aaaaagatga agaataccgc aaccatcgtg ataaataaca ggggtgcgta         240
aaatagcaaa acgcctcctg atgtcgccac ggctttaccg cctttaaatt tggcgaagat         300
gggaaacacg tggcctaaaa ccgcaaagac tcctgcaaga agcgggtgaa tatcaacatg         360
catgagaaaa ggcaatgcag ttgccagtgt ccctttcaaa atatctccgg ctatgacgac         420
cgaaccagct tttacaccca atgtacggaa tgcattggta gcgcctaagt tgccgcttcc         480
gtgctcccga atatcaattc ctttggcaag cttgcccaca attaagccag atggaatgct         540
gcctatcaag taggccaaaa taatcaataa agcaattaac at                           582
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